

Amendment to the Specification:

◇◇ Please replace the first paragraph (lines 1-15) on page 7 with the following amended paragraph:

lymphoid tumor cells representing a disease selected from B cell non-Hodgkin lymphoma, B cell lymphoma, B cell acute lymphoid leukemia, Burkitt lymphoma, Hodgkin lymphoma, hairy cell leukemia, acute myeloid leukemia, T cell lymphoma, T cell non-Hodgkin lymphoma, chronic myeloid leukemia, chronic lymphoid leukemia, and multiple myeloid leukemia. Exemplary activated lymphoid tumor cells which can be killed include PRIESS (ECACC Accession No: 86052111), GRANTA-519 (DSMZ Accession No: ACC 342), KARPAS-422 (DSMZ Accession No: ACC 32), KARPAS-299, DOHH-2, SR-786, MHH-CALL-4, MN-60, BJAB, RAJI, L-428, HDLM-2, HD-MY-Z, KM-H2, L1236, BONNA-12, HC-1, NALM-1, L-363, EOL-1, LP-1, RPMI-8226, and MHH-PREB-1 cell lines. In certain preferred embodiments, the subject compositions have an EC₅₀ of 100 nM or less, and preferably less than 10 nM or even 1 nM, for killing at least one of B cell lymphoma cells and T cell lymphoma cells selected from the list of KARPAS-422, DOHH-2, SR-786, MHH-CALL-4, MN-60, HD-MY-Z, NALM-1 and LP-1. In certain instances, to effect cell killing, the target cells may require further activation or pre-activation, such as by incubation with Lipopolysaccharide (LPS, 10 µg/ml), Interferon-gamma (IFN-γ, Roche, 40 ng/ml) and/or phyto-hemagglutinin (PHA, 5 µg/ml) to name but a few.

◇◇ Please replace lines 21-23 on page 9 with the following amended paragraph:

wherein each X independently represents any amino acid residue. For instance, the VH CDR3 sequence can be SPRYRGAFDY (SEQ ID No. 3) and/or the VL CDR3 sequence can be QSYDLIRH (SEQ ID No. 4) or QSYDMNVH (SEQ ID No. 5).

◇◇ Please replace lines 3-5 on page 10 with the following amended paragraph:

each X independently represents any amino acid residue. For instance, the VH CDR3 sequence can be SPRYRGAFDY (SEQ ID No. 3) and/or the VL CDR3 sequence can be QSYDLIRH (SEQ ID No. 4) or QSYDMNVH (SEQ ID No. 5).

◇◇ Please replace lines 22-23 on page 17 with the following amended paragraph:

For instance, the VH CDR3 sequence is SPRYRGAFDY (SEQ ID No. 3) and/or the VL CDR3 sequence is QSYDLIRH (SEQ ID No. 4) or QSYDMNVH (SEQ ID No. 5).

◇◇ Please replace lines 17-31 on page 38, lines 1-31 on page 38 and lines 1-6 on page 40 with the following amended text:

Figure 11 Vector map and sequence (SEQ ID NO: 33) of scFv phage display vector pMORPH13_scFv. The vector pMORPH13_scFv is a phagemid vector comprising a gene encoding a fusion between the C-terminal domain of the gene III protein of filamentous phage and a HuCAL scFv. In Figure 11, a vector comprising a model scFv gene (combination of VH1A and Vλ3 (Knappik et al., 2000) is shown. The original HuCAL master genes (Knappik et al. (2000): see Fig. 3 therein) have been constructed with their authentic N-termini: VH1A, VH1B, VH2, VH4 and VH6 with Q (=CAG) as the first amino acid. VH3 and VH5 with E (=GAA) as the first amino acid. Vector pMORPH13_scFv comprises the short FLAG peptide sequence (DYKD SEQ ID NO: 9) fused to the VH chain, and thus all HuCAL VH chains in, and directly derived from, this vector have E (=GAA) at the first position (e.g. in pMx7_FS vector, see Figure 12).

Figure 12 Vector map and sequence (SEQ ID NO: 34) of scFv expression vector pMx7_FS_5D2. The expression vector pMx7_FS_5D2 leads to the expression of HuCAL scFv fragments (in Figure 12, the vector comprises a gene encoding a "dummy" antibody fragment called "5D2") when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK SEQ ID NO: 8) (IBA GmbH, Göttingen, Germany; see: Schmidt and

Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997).

Figure 13 Vector map and sequence (SEQ ID NO: 35) of Fab expression vector pMx9_Fab_GPC8. The expression vector pMx9_Fab_GPC8 leads to the expression of HuCAL Fab fragments (in Figure 13, the vector comprises the Fab fragment MS-GPC8) when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK, SEQ ID No. 8) (IBA GmbH, Göttingen, Germany; see: Schmidt and Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997). In pMx9_Fab vectors, the HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position

Figure 14 Vector map and sequence (SEQ ID NO: 36) of Fab phage display vector pMORPH18_Fab_GPC8. The derivatives of vector pMORPH18 are phagemid vectors comprising a gene encoding a fusion between the C-terminal domain of the gene III protein of filamentous phage and the VH-CH1 chain of a HuCAL antibody. Additionally, the vector comprises the separately encoded VL-CL chain. In Figure 14, a vector comprising the Fab fragment MS-GPC-8 is shown. In pMORPH18_Fab vectors, the HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position.

Figure 15 Amino acid sequences of VH and VL domains of MS-GPC-1 (SEQ ID NOS 37[[-]] and 38, respectively), MS-GPC-6 (SEQ ID NOS 39[[-]] and 40, respectively), MS-GPC-8 (SEQ ID NOS 41[[-]] and 42, respectively), MS-GPC-10 (SEQ ID NOS 43[[-]] and 44, respectively), MS-GPC-8-6 (SEQ ID NOS 41 and 45-46, respectively), MS-GPC-8-10 (SEQ ID NOS 41 and 47-48, respectively), MS-GPC-8-17 (SEQ ID NOS 41 and 49-50, respectively), MS-GPC-8-27 (SEQ ID NOS 41 and 51-52, respectively), MS-GPC-8-6-13 (SEQ ID NOS 41 and 53-54, respectively), MS-GPC-

8-10-57 (SEQ ID NOS 41 and 55-56, respectively), ~~and~~ MS-GPC-8-27-41 (SEQ ID NOS 41 and 57-58, respectively), MS-GPC-8-1 (SEQ ID NOS 41 and 28, respectively), MS-GPC-8-9 (SEQ ID NOS 41 and 31, respectively), MS-GPC-8-18 (SEQ ID NOS 41 and 32, respectively), MS-GPC-8-6-2 (SEQ ID NOS 41 and 45, respectively), MS-GPC-8-6-19 (SEQ ID NOS 41 and 47, respectively), MS-GPC-8-6-27 (SEQ ID NOS 41 and 49, respectively), MS-GPC-8-6-45 (SEQ ID NOS 41 and 51, respectively), MS-GPC-8-6-47 (SEQ ID NOS 41 and 53, respectively), MS-GPC-8-27-7 (SEQ ID NOS 41 and 55, respectively), and MS-GPC-8-27-10 (SEQ ID NOS 41 and 57, respectively). The sequences in Figure 15 show amino acid 1 of VH as constructed in the original HuCAL master genes (Knappik et al. (2000): see Fig. 3 therein). In scFv constructs, as described in this application, amino acid 1 of VH is always E (see figure caption of Figure 11), in Fab constructs as described in this application, amino acid 1 of VH is always Q (see figure caption of Figure 13).

◇◇ Please replace Table 1 and 2 on pages 77-79, in Tables 1 and 2 with the following amended Table 1 and 2:

Table 1:

VH and VL families, VL CDR1 and VH/VL CDR 3 sequences of HLA-DR-specific polypeptides

Clone	VH	CDR3 Length	VH-CDR3-Seq.	VL	VL-CDR1-Seq.	CDR3 Length	VL-CDR3-Seq.	Families
MS-GPC-1	H2	10	QYCHRGFDH (SEQ ID NO: 19)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDFNES (SEQ ID NO: 63)	H2 λ 1
MS-GPC-6	H3	9	GYGRYSPDL (SEQ ID NO: 20)	K3	RASQSVSSSYLA (SEQ ID NO: 6259)	8	QQYSNLPF (SEQ ID NO: 21)	H3 K 3
MS-GPC-8	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDMPQA (SEQ ID NO: 22)	H2 λ 1
MS-GPC-10	H2	10	QLHYRGGFDL (SEQ ID NO: 61)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDLTMG (SEQ ID NO: 23)	H2 λ 1
MS-GPC-8-1	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDFSHY (SEQ ID NO: 24)	H2 λ 1
MS-GPC-8-6	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-9	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDIQLH (SEQ ID NO: 25)	H2 λ 1
MS-GPC-8-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDLIRH (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-17	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDFSIV (SEQ ID NO: 26)	H2 λ 1
MS-GPC-8-18	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDFSIV (SEQ ID NO: 27)	H2 λ 1
MS-GPC-8-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1

MS-GPC-8-6-2	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVH (SEQ ID NO: 13)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-19	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVA (SEQ ID NO: 14)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSDSNIGANYVT (SEQ ID NO: 15)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-45	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSEPNIGSNYVF (SEQ ID NO: 2816)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-13	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVT (SEQ ID NO: 29)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-47	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVS (SEQ ID NO: 30)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-10-57	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYYVQ (SEQ ID NO: 7)	8	QSYDLIRH (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-27-7	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYYVG (SEQ ID NO: 317)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVN (SEQ ID NO: 3218)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-41	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYYVQ (SEQ ID NO: 7)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1

Table 2:

Steps in Antibody optimisation	Fab	$k_{on} [s^{-1}M^{-1}] \times 10^5$ + SD	$k_{off} [s^{-1}] \times 10^{-3}$ + SD	$K_D [nM]$ + SD	L-CDR3	L-CDR1
Parental Fab	MS-GPC-8	0.99 ± 0.40	29.0 ± 8.40	$346.1 \pm 140.5^a)$	QSYDMPQA (SEQ ID NO: 22)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3-optim.	-8-1	1.93	20.9	108 ^{e)}		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	$58.6 \pm 11.7^b)$		
L-CDR3-optim.	-8-9	1.85	16.6	90.1 ^{e)}		
L-CDR3-optim.	-8-10	nd	7.0 ^{e)}	nd		
L-CDR3-optim.	-8-17	1.0	5.48	54.7 ^{e)}		
L-CDR3-optim.	-8-18	1.06	8.3	78.3 ^{e)}		
L-CDR3-optim.	-8-27	nd	6.6 ^{e)}	nd		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	$58.6 \pm 11.7^b)$	QSYDYDHY (SEQ ID NO: 60)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3+1-opt.	-8-6-2	1.23 ± 0.11	0.94 ± 0.07	$7.61 \pm 0.25^c)$	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVH (SEQ ID NO: 13)
L-CDR3+1-opt.	-8-6-19	1.10 ± 0.08	0.96 ± 0.15	$8.74 \pm 1.33^c)$	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVA (SEQ ID NO: 14)
L-CDR3+1-opt.	-8-6-27	1.80 ± 0.24	1.10 ± 0.15	$6.30 \pm 0.63^d)$	QSYDYDHY (SEQ ID NO: 60)	SGSDSNIGANYVT (SEQ ID NO: 15)
L-CDR3+1-opt.	-8-6-45	1.20 ± 0.07	1.03 ± 0.04	$8.63 \pm 0.61^e)$	QSYDYDHY	SGSEP NIGSNYVF

					(SEQ ID NO: 60)	(SEQ ID NO: 16)
L-CDR3+1-opt.	-8-6-13	1.90 ± 0.26	0.55 ± 0.05	2.96 ± 0.46 ^{c)}	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGANYVT (SEQ ID NO: 1529)
L-CDR3+1-opt.	-8-6-47	1.97 ± 0.29	0.62 ± 0.04	3.18 ± 0.33 ^{c)}	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVS (SEQ ID NO: 1230)
L-CDR3+1-opt.	-8-10-57	1.65 ± 0.21	0.44 ± 0.06	2.67 ± 0.25 ^{c)}	QSYDLIRH (SEQ ID NO: 4)	SGSESNIGNNYVQ (SEQ ID NO: 7)
L-CDR3+1-opt.	-8-27-7	1.74 ± 0.21	0.57 ± 0.07	3.30 ± 0.34 ^{d)}	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVG (SEQ ID NO: 17)
L-CDR3+1-opt.	-8-27-10	1.76 ± 0.21	0.53 ± 0.05	3.01 ± 0.21 ^{c)}	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGANYVN (SEQ ID NO: 18)
L-CDR3+1-opt.	-8-27-41	1.67 ± 0.16	0.49 ± 0.03	2.93 ± 0.27 ^{d)}	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVQ (SEQ ID NO: 7)

a) Affinity data of MS-GPC-8 are based on 8 different Fab-preparations which were measured on 4 different chips (2 x 500, 1000, 4000RU)

b) For MS-GPC-8-6 mean and standard deviation of 3 different preparations on 3 different chips (500, 4000, 3000RU) is shown.

c) 3000RU MHCII were immobilized on a CM5-chip. For each measurement 7 different concentrations from 1µM to 16nM were injected on the surface. Dissociation time: 150sec, regeneration was reached by 6µl 10mM Glycine pH2.3 followed by 8µl 7.5mM NaOH. For MS-GPC-8-6-19 mean and standard deviation of 4 different preparations are shown whereas for all other binders mean and standard deviation of 3 different preparations are shown.

d) One protein preparation is measured on 3 different chips (3000, 2800 and 6500RU).

e) Affinity determination of matured MHCII binder on a 4000RU density chips; single measurement.

Molecular weights were determined after size exclusion chromatography and found 100% monomeric with the right molecular weight between 45 and 48 kDa.

◇◇ Please replace Figure 15 with the following amended Figure 15:

Figure 15

MS-GPC-1:

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
QYGHRGGFDHWGQGTLVTVSS (SEQ ID NO: 37)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSGKSGTSASLAITGLQSEDEADYYCQSYDFNESVF
GGGTKLTVLG (SEQ ID NO: 38)

MS-GPC-6

VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWV
SAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR
GYGRYSPDLWGQGTLVTVSS (SEQ ID NO: 39)

VL

DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY
GASSRATGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNLPFTFG
QGTKVEIKRT (SEQ ID NO: 40)

MS-GPC-8

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMPQAV
FGGGTKLTVLG (SEQ ID NO: 42)

MS-GPC-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR
QLHYRGGFDLWGQGTLVTVSS (SEQ ID NO: 43)

VL

DIVLTQPPSVSGAPGQRTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLTMGVF
GGGTKLTVLG (SEQ ID NO: 44)

MS-GPC-8-6

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF
GGGTKLTVLG (SEQ ID NO: 46)

MS-GPC-8-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF
GGGTKLTVLG (SEQ ID NO: 48)

MS-GPC-8-17

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSVYVF
GGGTKLTVLG (SEQ ID NO: 50)

MS-GPC-8-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV
FGGGTKLTVLG (SEQ ID NO: 52)

MS-GPC-8-6-13

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSESNIGANYVTWYQQLPGTAPKLLIYD
NNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG
GGTKLTVLG (SEQ ID NO: 54)

MS-GPC-8-10-57

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF
GGGTKLTVLG (SEQ ID NO: 56)

MS-GPC-8-27-41

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV
FGGGTKLTVLG (SEQ ID NO: 58)

MS-GPC-8-1

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSHYVF
GGGTKLTVLG (SEQ ID NO:28)

MS-GPC-8-9

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDIQLHVF
GGGTKLTVLG (SEQ ID NO: 31)

MS-GPC-8-18

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVL TMTNMDPVD TATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSIIYVF
GGGTKLTVLG (SEQ ID NO: 32)

MS-GPC-8-6-2

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVL TMTNMDPVD TATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVHWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF
GGGTKLTVLG (SEQ ID NO: 45)

MS-GPC-8-6-19

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVL TMTNMDPVD TATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSESNIGSNYVAWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF
GGGTKLTVLG (SEQ ID NO: 47)

MS-GPC-8-6-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSDSNIGANYVTWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF
GGGTKLTVLG (SEQ ID NO: 49)

MS-GPC-8-6-45

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSEPNIGSNYVFWYQQLPGTAPKLLIYD
NNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG
GGTKLTVLG (SEQ ID NO: 51)

MS-GPC-8-6-47

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVSWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF
GGGTKLTVLG (SEQ ID NO: 53)

MS-GPC-8-27-7

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVGWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV
FGGGTKLTVLG (SEQ ID NO: 55)

MS-GPC-8-27-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTISCSGSESNIGANYVNWYQQLPGTAPKLLIY
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV
FGGGTKLTVLG (SEQ ID NO: 57)